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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/910,706A

DATE: 03/13/2002

TIME: 11:16:34

Input Set : A:\JHU1520-2.TXT

Output Set: N:\CRF3\03132002\I910706A.raw

4 <110> APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
 5 WORLEY, Paul F.  
 6 BRAKEMAN, Paul R.  
 8 <120> TITLE OF INVENTION: SYNAPTIC ACTIVATION PROTEIN COMPOSITIONS AND METHOD  
 10 <130> FILE REFERENCE: JHU1520-2  
 12 <140> CURRENT APPLICATION NUMBER: US 09/910,706A  
 13 <141> CURRENT FILING DATE: 2001-07-20  
 15 <150> PRIOR APPLICATION NUMBER: US 09/042,428  
 16 <151> PRIOR FILING DATE: 1998-03-13  
 18 <150> PRIOR APPLICATION NUMBER: US 60/036,553  
 19 <151> PRIOR FILING DATE: 1997-03-14  
 21 <160> NUMBER OF SEQ ID NOS: 15  
 23 <170> SOFTWARE: PatentIn version 3.0  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 558  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: Rattus norvegicus  
 30 <220> FEATURE:  
 31 <221> NAME/KEY: CDS  
 32 <222> LOCATION: (1)...(558)  
 34 <400> SEQUENCE: 1  
 35 atg ggg gaa caa cct atc ttc agc act cga gct cat gtc ttc cag atc 48  
 36 Met Gly Glu Gln Pro Ile Phe Ser Thr Arg Ala His Val Phe Gln Ile  
 37 1 5 10 15  
 39 gac cca aac aca aag aac tgg gta ccc acc agc aag cat gca gtt 96  
 40 Asp Pro Asn Thr Lys Lys Asn Trp Val Pro Thr Ser Lys His Ala Val  
 41 20 25 30  
 43 act gtg tct tat ttc tat gac agc aca agg aat gtg tat agg ata atc 144  
 44 Thr Val Ser Tyr Phe Tyr Asp Ser Thr Arg Asn Val Tyr Arg Ile Ile  
 45 35 40 45  
 47 agt cta gac ggc tca aag gca ata ata aat agc acc atc act cca aac 192  
 48 Ser Leu Asp Gly Ser Lys Ala Ile Ile Asn Ser Thr Ile Thr Pro Asn  
 49 50 55 60  
 51 atg aca ttt act aaa aca tct caa aag ttt ggc caa tgg gct gat agc 240  
 52 Met Thr Phe Thr Lys Thr Ser Gln Lys Phe Gly Gln Trp Ala Asp Ser  
 53 65 70 75 80  
 55 cgg gca aac act gtt tat gga ctg gga ttc tcc tct gag cat cat ctc 288  
 56 Arg Ala Asn Thr Val Tyr Gly Leu Gly Phe Ser Ser Glu His His Leu  
 57 85 90 95  
 59 tca aaa ttt gca gaa aag ttt cag gaa ttt aaa gaa gct gct cgg ctg 336  
 60 Ser Lys Phe Ala Glu Lys Phe Gln Glu Phe Lys Glu Ala Ala Arg Leu  
 61 100 105 110  
 63 gca aag gag aag tcg cag gag aag atg gaa ctg acc agt acc cct tca 384

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64 Ala Lys Glu Lys Ser Gln Glu Lys Met Glu Leu Thr Ser Thr Pro Ser  
 65 115 120 125  
 67 cag gaa tca gca gga gga gat ctt cag tct cct tta aca cca gaa agt 432  
 68 Gln Glu Ser Ala Gly Gly Asp Leu Gln Ser Pro Leu Thr Pro Glu Ser  
 69 130 135 140  
 71 atc aat ggg aca gat gat gag aga aca ccc gat gtg aca cag aac tca 480  
 72 Ile Asn Gly Thr Asp Asp Glu Arg Thr Pro Asp Val Thr Gln Asn Ser  
 73 145 150 155 160  
 75 gag cca agg gct gag cca gct cag aat gca ttg cca ttt tca cat agg 528  
 76 Glu Pro Arg Ala Glu Pro Ala Gln Asn Ala Leu Pro Phe Ser His Arg  
 77 165 170 175  
 79 tac aca ttc aat tca gca atc atg att aaa  
 80 Tyr Thr Phe Asn Ser Ala Ile Met Ile Lys 558  
 81 180 185  
 84 <210> SEQ ID NO: 2  
 85 <211> LENGTH: 186  
 86 <212> TYPE: PRT  
 87 <213> ORGANISM: Rattus norvegicus  
 89 <400> SEQUENCE: 2  
 91 Met Gly Glu Gln Pro Ile Phe Ser Thr Arg Ala His Val Phe Gln Ile  
 92 1 5 10 15  
 93 Asp Pro Asn Thr Lys Lys Asn Trp Val Pro Thr Ser Lys His Ala Val  
 94 20 25 30  
 95 Thr Val Ser Tyr Phe Tyr Asp Ser Thr Arg Asn Val Tyr Arg Ile Ile  
 96 35 40 45  
 97 Ser Leu Asp Gly Ser Lys Ala Ile Ile Asn Ser Thr Ile Thr Pro Asn  
 98 50 55 60  
 99 Met Thr Phe Thr Lys Thr Ser Gln Lys Phe Gly Gln Trp Ala Asp Ser  
 100 65 70 75 80  
 101 Arg Ala Asn Thr Val Tyr Gly Leu Gly Phe Ser Ser Glu His His Leu  
 102 85 90 95  
 103 Ser Lys Phe Ala Glu Lys Phe Gln Glu Phe Lys Glu Ala Ala Arg Leu  
 104 100 105 110  
 105 Ala Lys Glu Lys Ser Gln Glu Lys Met Glu Leu Thr Ser Thr Pro Ser  
 106 115 120 125  
 107 Gln Glu Ser Ala Gly Gly Asp Leu Gln Ser Pro Leu Thr Pro Glu Ser  
 108 130 135 140  
 109 Ile Asn Gly Thr Asp Asp Glu Arg Thr Pro Asp Val Thr Gln Asn Ser  
 110 145 150 155 160  
 111 Glu Pro Arg Ala Glu Pro Ala Gln Asn Ala Leu Pro Phe Ser His Arg  
 112 165 170 175  
 113 Tyr Thr Phe Asn Ser Ala Ile Met Ile Lys  
 114 180 185  
 116 <210> SEQ ID NO: 3  
 117 <211> LENGTH: 50  
 118 <212> TYPE: PRT  
 119 <213> ORGANISM: Homo sapiens  
 121 <400> SEQUENCE: 3  
 123 Met Gly Glu Gln Pro Ile Phe Thr Thr Arg Ala His Val Phe Gln Ile

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124 1 5 10 15  
125 Asp Pro Asn Thr Lys Lys Asn Trp Met Pro Ala Ser Lys His Gly His  
126 20 25 30  
127 Arg Phe Tyr Phe Tyr Asp Val Thr Arg Asn Ser Tyr Arg Ile Ile Ser  
128 35 40 45  
129 Val Asp  
130 50  
132 <210> SEQ ID NO: 4  
133 <211> LENGTH: 153  
134 <212> TYPE: PRT  
135 <213> ORGANISM: Mus musculus  
137 <400> SEQUENCE: 4  
139 Tyr Phe Tyr Asp Val Thr Arg Asn Ser Tyr Arg Ile Ile Ser Val Asp  
140 1 5 10 15  
141 Gly Ala Lys Val Ile Ile Asn Ser Thr Ile Thr Pro Asn Met Thr Phe  
142 20 25 30  
143 Thr Lys Thr Ser Gln Lys Phe Gly Gln Trp Ala Asp Ser Arg Ala Asn  
144 35 40 45  
145 Thr Val Phe Gly Leu Gly Phe Ser Ser Glu Leu Gln Leu Thr Lys Phe  
146 50 55 60  
147 Ala Glu Lys Phe Gln Glu Val Arg Glu Ala Ala Arg Leu Ala Arg Asp  
148 65 70 75 80  
149 Lys Ser Gln Glu Lys Thr Glu Thr Ser Ser Asn His Ser Gln Glu Ser  
150 85 90 95  
151 Gly Cys Glu Thr Pro Ser Ser Thr Gln Ala Ser Ser Val Asn Gly Thr  
152 100 105 110  
153 Asp Asp Glu Lys Ala Ser His Ala Ser Pro Ala Asp Thr His Leu Lys  
154 115 120 125  
155 Ser Glu Asn Asp Lys Leu Lys Ile Ala Leu Thr Gln Ser Ala Ala Asn  
156 130 135 140  
157 Val Lys Lys Trp Glu Met Glu Leu Gln  
158 145 150  
160 <210> SEQ ID NO: 5  
161 <211> LENGTH: 10  
162 <212> TYPE: PRT  
163 <213> ORGANISM: Artificial sequence  
165 <220> FEATURE:  
166 <223> OTHER INFORMATION: C-terminal of metabotropic glutamate receptor,  
167 mGluR1-alpha.  
169 <400> SEQUENCE: 5  
171 Arg Asp Tyr Lys Gln Ser Ser Ser Thr Leu  
172 1 5 10  
174 <210> SEQ ID NO: 6  
175 <211> LENGTH: 10  
176 <212> TYPE: PRT  
177 <213> ORGANISM: Artificial sequence  
179 <220> FEATURE:  
180 <223> OTHER INFORMATION: C-terminal of metabotropic glutamate receptor,  
181 mGluR2.

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183 <400> SEQUENCE: 6  
184 Glu Val Val Asp Ser Thr Thr Ser Ser Leu  
185 1 5 10  
187 <210> SEQ ID NO: 7  
188 <211> LENGTH: 10  
189 <212> TYPE: PRT  
190 <213> ORGANISM: Artificial sequence  
192 <220> FEATURE:  
193 <223> OTHER INFORMATION: C-terminal of metabotropic glutamate receptor,  
194 mGluR3.  
196 <400> SEQUENCE: 7  
198 Glu Val Leu Asp Ser Thr Thr Ser Ser Leu  
199 1 5 10  
201 <210> SEQ ID NO: 8  
202 <211> LENGTH: 10  
203 <212> TYPE: PRT  
204 <213> ORGANISM: Artificial sequence  
206 <220> FEATURE:  
207 <223> OTHER INFORMATION: C-terminal of metabotropic glutamate receptor,  
208 mGluR4.  
210 <400> SEQUENCE: 8  
212 Thr Tyr Val Thr Tyr Thr Asn His Ala Ile  
213 1 5 10  
215 <210> SEQ ID NO: 9  
216 <211> LENGTH: 10  
217 <212> TYPE: PRT  
218 <213> ORGANISM: Artificial sequence  
220 <220> FEATURE:  
221 <223> OTHER INFORMATION: C-terminal of metabotropic glutamate receptor,  
222 mGluR5.  
224 <400> SEQUENCE: 9  
226 Arg Asp Tyr Thr Gln Ser Ser Ser Ser Leu  
227 1 5 10  
229 <210> SEQ ID NO: 10  
230 <211> LENGTH: 4  
231 <212> TYPE: PRT  
232 <213> ORGANISM: Artificial sequence  
234 <220> FEATURE:  
235 <223> OTHER INFORMATION: peptide binding sequence  
237 <400> SEQUENCE: 10  
238 Ser Ser Thr Leu  
239 1  
241 <210> SEQ ID NO: 11  
242 <211> LENGTH: 4  
243 <212> TYPE: PRT  
244 <213> ORGANISM: Artificial sequence  
246 <220> FEATURE:  
247 <223> OTHER INFORMATION: peptide binding sequence  
249 <400> SEQUENCE: 11

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251 Ser Ser Ser Leu  
252 1  
254 <210> SEQ ID NO: 12  
255 <211> LENGTH: 4  
256 <212> TYPE: PRT  
257 <213> ORGANISM: Rattus norvegicus  
259 <220> FEATURE:  
260 <221> NAME/KEY: VARIANT  
261 <222> LOCATION: (0)...(0)  
262 <223> OTHER INFORMATION: position 31-34 of SEQ ID NO:2  
264 <400> SEQUENCE: 12  
266 Ala Val Thr Val  
267 1  
269 <210> SEQ ID NO: 13  
270 <211> LENGTH: 4  
271 <212> TYPE: PRT  
272 <213> ORGANISM: Homo sapiens / Mouse  
274 <220> FEATURE:  
275 <221> NAME/KEY: VARIANT  
276 <222> LOCATION: (0)...(0)  
277 <223> OTHER INFORMATION: positions 31-34 of SEQ ID NO:3  
279 <400> SEQUENCE: 13  
281 Gly His Arg Phe  
282 1  
284 <210> SEQ ID NO: 14  
285 <211> LENGTH: 4  
286 <212> TYPE: PRT  
287 <213> ORGANISM: Artificial Sequence  
289 <220> FEATURE:  
290 <223> OTHER INFORMATION: PDZ-like domain  
292 <400> SEQUENCE: 14  
294 Gly Leu Gly Phe  
295 1  
297 <210> SEQ ID NO: 15  
298 <211> LENGTH: 4  
299 <212> TYPE: PRT  
300 <213> ORGANISM: Artificial Sequence  
302 <220> FEATURE:  
303 <223> OTHER INFORMATION: C-terminal motif  
305 <400> SEQUENCE: 15  
307 Thr Ser Ser Leu  
308 1

**VERIFICATION SUMMARY**

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